

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 17, 2006, 17:50:39 ; Search time 193 Seconds
(without alignments)
2160.469 Million cell updates/sec

Title: US-10-667-281-2

Perfect score: 5183
Sequence: 1 GNHRAFGSRSPGVPTLL.....CDPLKKRHFIDFCTMAECS 949

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

- A_Geneseq_21:*
- 1: geneseqp1980s:*
 - 2: geneseqp1990s:*
 - 3: geneseqp2000s:*
 - 4: geneseqp2001s:*
 - 5: geneseqp2002s:*
 - 6: geneseqp2003as:*
 - 7: geneseqp2003bs:*
 - 8: geneseqp2004s:*
 - 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5183	100.0	949	7	ADG72483
2	5183	100.0	949	9	ADG72483 Human agg
3	5183	100.0	950	9	ADG72483 Human agg
4	5174	99.8	950	8	ADG72483 Human agg
5	5174	99.8	950	8	ADG72483 Human agg
6	5174	99.8	950	8	ADG72483 Human agg
7	5174	99.8	950	8	ADG72483 Human agg
8	5174	99.8	950	8	ADG72483 Human agg
9	5174	99.8	950	8	ADG72483 Human agg
10	5169	99.7	950	2	ADG72483 Human agg

ALIGNMENTS

RESULT 1
ID ADG72483 standard; protein; 949 AA.
XX
AC ADG72483;
DT 11-MAR-2004 (first entry)
XX
DE Human aggrecanase (ADAMTS-1).

XX	Human; aggrecanase; ADAMTS-1; rheumatoid arthritis; osteoarthritis;
KM	antiarthritic; osteopathic; enzyme.
XX	
OS	Homo sapiens.
XX	
PN	US6649377-B1.
XX	
PD	18-NOV-2003.
XX	
PF	09-MAY-2000; 2000US-00566559.
XX	
PR	10-MAY-1999; 99US-0133343P.
XX	
PA	(SYNT) SYNTAX USA LLC.
XX	
PI	Allard JD, Heller RA, Klonowski P, Vanwart HE,
XX	
DR	WPI; 2003-896162/82.
XX	
DR	N-PSDB; ADG72482.
XX	
PT	New nucleic acid present in other than its natural environment, useful
PT	for preparing a composition for diagnosing or treating diseases
PT	associated with aggrecanase activity, e.g. rheumatoid arthritis or
PT	osteoarthritis.
PS	Disclosure; SEQ ID NO 2; 26pp; English.
XX	
CC	The present invention relates to the isolation of human aggrecanase
CC	(ADAMTS-1), and the polynucleotide sequence encoding it. Also disclosed
CC	are a method of producing aggrecanase in vitro. The polynucleotide
CC	sequence encoding aggrecanase is useful for preparing a composition for
CC	diagnosing or treating diseases associated with aggrecanase activity e.g.
CC	rheumatoid arthritis or osteoarthritis. The present sequence represents
CC	human aggrecanase.
XX	
XX	Sequence 949 AA;
XX	
Query Match	100.0%; Score 5183; DB 7; Length 949;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 949; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GNHRAFGSRSPGVPTLLAAALAVSDALGRPEDEBELVPELEAPAGHTTRRL 60
DB	1 GNHRAFGSRSPGVPTLLAAALAVSDALGRPEDEBELVPELEAPAGHTTRRL 60
QY	61 HAFDQDLLELRPDSSFLAPGFTLQNVGRKSGSETPLEPTDLAHCYSGTVNDPSSAAA 120
DB	61 HAFDQDLLELRPDSSFLAPGFTLQNVGRKSGSETPLEPTDLAHCYSGTVNDPSSAAA 120
QY	121 LSLGSGVRGAFYLLGHAFTYIQLPAASERLATAPSEKPPAPLOFTLLRRNGDVGTC 180
DB	121 LSLGSGVRGAFYLLGHAFTYIQLPAASERLATAPSEKPPAPLOFTLLRRNGDVGTC 180
QY	181 GVNDPEPRPTGAEFTDEDEGTEGEDEGQWSPDAPALGVGQPTGTGIRKKRFVSSHR 240
DB	181 GVNDPEPRPTGAEFTDEDEGTEGEDEGQWSPDAPALGVGQPTGTGIRKKRFVSSHR 240
QY	241 YVETMLVADQSNVAEFHSGGLKHYLLTFSVAARLYKHPISIRNSVSLVVKILIVHEQKG 300
DB	241 YVETMLVADQSNVAEFHSGGLKHYLLTFSVAARLYKHPISIRNSVSLVVKILIVHEQKG 300
QY	301 PEVTSNAALTTLNFCNWKQKPNPSPDRDAEHYDTAILFTRODLCGSGTCDDTLGMAADVTV 360
DB	301 PEVTSNAALTTLNFCNWKQKPNPSPDRDAEHYDTAILFTRODLCGSGTCDDTLGMAADVTV 360
QY	361 CDPSSRCVTEDDGQAAFTTAHELGHPNMHPDAPKQASLNGVNDSHMAASMLSNID 420
DB	361 CDPSSRCVTEDDGQAAFTTAHELGHPNMHPDAPKQASLNGVNDSHMAASMLSNID 420
QY	421 HSQWSPSCAYWITSLFNGHGECLMDKRPNDIQLPGDLPGTSYDANRCQPTFGEDSKH 480
DB	421 HSQWSPSCAYWITSLFNGHGECLMDKRPNDIQLPGDLPGTSYDANRCQPTFGEDSKH 480

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OM protein - protein search, using sw model

Run on: March 17, 2006, 17:58:35 ; Search time 49 Seconds
(without alignments)
1601.209 Million cell updates/sec

Title: US-10-667-281-2

Sequence: 1 GNAERAPGSRSGFPVPTLL.....CDPLKKPKHIDECTMAECS 949

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 10 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/aa/5 COMB.pep:*
2: /cgn2_6/prodata/1/aa/6 COMB.pep:*
3: /cgn2_6/prodata/1/aa/H COMB.pep:*
4: /cgn2_6/prodata/1/aa/PTUS COMB.pep:*
5: /cgn2_6/prodata/1/aa/RB COMB.pep:*
6: /cgn2_6/prodata/1/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5183	100.0	949	2	US-09-568-559-2
2	5169	99.7	967	2	US-09-130-491-2
3	4287.5	82.7	950	2	US-09-321-987B-4
4	3940	76.0	727	2	US-09-445-023A-1
5	3674	70.9	727	2	US-09-445-023A-12
6	3315	64.0	608	2	US-09-130-491-13
7	2812	54.3	551	2	US-09-130-491-16
8	2480.5	47.9	950	2	US-10-009-332-1
9	2332	45.0	887	2	US-09-949-002-534
10	2331.5	45.0	890	2	US-09-949-002-394

ALIGNMENTS

RESULT 1
US-09-568-559-2
; Sequence 2, Application US/09568559
; Patent No. 6649377
; GENERAL INFORMATION:
; APPLICANT: Klonowski, Paul
; APPLICANT: Allard, John
; APPLICANT: Heller, Renu
; APPLICANT: Van Wart, Harold
; TITLE OF INVENTION: Human Aggrecanase and Nucleic Acid
; FILE REFERENCE: ROCH-002

CURRENT APPLICATION NUMBER: US/09/568,559
; CURRENT FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/133,343
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 949
; TYPE: PRT
; ORGANISM: human
US-09-568-559-2
Query Match 100.0%; Score 5183; DB 2; Length 949;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 949; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GNAERAPGSRSGFPVPTLLAAALAVSALGRPSREDELYVPELRAPGHGTTLR 60
DB 1 GNAERAPGSRSGFPVPTLLAAALAVSALGRPSREDELYVPELRAPGHGTTLR 60
QY 61 HAPDQDLERLPPDSFIAPGFTLONVGRSGSETPLPETDLACFYSGTVNGDPSSAAA 120
DB 61 HAPDQDLERLPPDSFIAPGFTLONVGRSGSETPLPETDLACFYSGTVNGDPSSAAA 120
QY 121 LSLCEGVGAFFYLGEAYFIQPLPAASERLATAPEGKPPAPIQFILLRRNRQDVGATC 180
DB 121 LSLCEGVGAFFYLGEAYFIQPLPAASERLATAPEGKPPAPIQFILLRRNRQDVGATC 180
QY 121 LSLCEGVGAFFYLGEAYFIQPLPAASERLATAPEGKPPAPIQFILLRRNRQDVGATC 180
DB 121 LSLCEGVGAFFYLGEAYFIQPLPAASERLATAPEGKPPAPIQFILLRRNRQDVGATC 180
QY 181 GVVDEPRPTGKATEDEDEDETEGEDEGAQWSQODPALQGVQPTGTGIRKRFVSSHR 240
DB 181 GVVDEPRPTGKATEDEDEDETEGEDEGAQWSQODPALQGVQPTGTGIRKRFVSSHR 240
QY 241 YVETMLVADQSMARFPGSGIKHYLLTLFSVAALRYKPSIRNSVILVVVILVHDSOKG 300
DB 241 YVETMLVADQSMARFPGSGIKHYLLTLFSVAALRYKPSIRNSVILVVVILVHDSOKG 300
QY 301 PEVTSNAALTIRNFCNWKQKHPNSDRDAEHVDTALLFTRODLCSQTCDTLGNADVTV 360
DB 301 PEVTSNAALTIRNFCNWKQKHPNSDRDAEHVDTALLFTRODLCSQTCDTLGNADVTV 360
QY 361 CDPSSRCSTVEDDGLQAAFTTAHELGHVFMPPHDDAKQCSLNGVNDSSHMASSLNLD 420
DB 361 CDPSSRCSTVEDDGLQAAFTTAHELGHVFMPPHDDAKQCSLNGVNDSSHMASSLNLD 420
QY 421 HSQWSPCSAYMTSTFLDNGHGCIMDKPQNPLOLGEDLPSTYDAROCQFTGEBSKH 480
DB 421 HSQWSPCSAYMTSTFLDNGHGCIMDKPQNPLOLGEDLPSTYDAROCQFTGEBSKH 480
QY 481 CPDPAASTCTLMCTGTSGLVLCOTKHFPPADGTSCEGKMCINGKCVNKTTHRGHPTPF 540
DB 481 CPDPAASTCTLMCTGTSGLVLCOTKHFPPADGTSCEGKMCINGKCVNKTTHRGHPTPF 540
QY 541 HGSWMGMPWGDSCRTCGGQVQYTMBCDNPVRNGKTCYEGKRVYRSQNLBDCPDNG 600
DB 541 HGSWMGMPWGDSCRTCGGQVQYTMBCDNPVRNGKTCYEGKRVYRSQNLBDCPDNG 600
QY 601 KTFREOCCEAHNFPSASRSGSPAVEMIPKCAVSPDRCKLCOAGIGIFFLQKRV 660
DB 601 KTFREOCCEAHNFPSASRSGSPAVEMIPKCAVSPDRCKLCOAGIGIFFLQKRV 660
QY 661 DGTFCSPDSTVCGQCCVAGCDRIIDSKKKDKCGVCGGNGSTCKKISGVSATRGY 720
DB 661 DGTFCSPDSTVCGQCCVAGCDRIIDSKKKDKCGVCGGNGSTCKKISGVSATRGY 720
QY 721 HDITITPTGATNIEVKQRNQRSGRNGSFLAIAADGTYLNGDYTLSTBEDIMYGVV 780
DB 721 HDITITPTGATNIEVKQRNQRSGRNGSFLAIAADGTYLNGDYTLSTBEDIMYGVV 780
QY 781 LRYSGSSALLERIRSSPLKEPLTIQVLTGMLRPKIKTYVKKKKSSFNAIPTFSAW 840
DB 781 LRYSGSSALLERIRSSPLKEPLTIQVLTGMLRPKIKTYVKKKKSSFNAIPTFSAW 840
QY 841 VIREMGCKSKCBLQGRRLVECRDINGQPASECAYKVPASTRPCADHPQWOLGWS 900

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OM protein - protein search, using sw model

Run on: March 17, 2006, 17:54:29 ; Search time 48 Seconds
(without alignments)
1902.286 Million cell updates/sec

Title: US-10-667-281-2
Perfect score: 5183
Sequence: 1 GNAERAPGSRSGFVPTLL.....CDPLKKRHPIDFCMAECS 949

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 10 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4291.5	82.8	951	2 T00017	gene ADAMTS-1 prot
2	3074	59.3	530	2 T47158	hypothetical prote
3	2136	41.2	837	2 T00355	hypothetical prote
4	1613	31.1	2165	2 T21371	hypothetical prote
5	1118	21.6	1205	2 T18517	procollagen N-endo
6	647	12.5	1558	2 C89114	protein C37C3.6a f
7	647	12.5	2167	2 T34395	hypothetical prote
8	634.5	12.2	1444	2 T18856	angiogenesis inhib
9	475	9.2	860	2 T16892	hypothetical prote
10	424.5	8.2	1059	2 T22545	hypothetical prote

ALIGNMENTS

RESULT 1
T00017
gene ADAMTS-1 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 15-Mar-2004
C:Accession: T00017
R:Kuno, K.; Lizaas, H.; Ohno, S.; Matsushima, K.
Genomic 46, 466-471, 1997
A:Title: The exon/intron organization and chromosomal mapping of the mouse ADAMTS-1 gene
A:Reference number: Z14055, MUID:99110583, PMID:9441751
A:Accession: T00017
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-951 <KUN>

A:Cross-references: UNIPARC:UP10000049F23; EMBL:AB001735; NID:G2809056; PIDN:BA24501.
A:Experimental source: strain 129SVJ
C:Genetics:
A:Gene: ADAMTS-1
A:Introns: 228/1; 343/3; 388/1; 444/1; 539/3; 602/1; 660/3; 719/2
F:542-598/Domain: thrombospondin type 1 repeat homology <THR3>

Query Match 82.8% Score 4291.5; DB 2; Length 951;
Best Local Similarity 82.3%; Pred. No. 3.5e-266;
Matches 788; Conservative 55; Mismatches 99; Indels 15; Gaps 5;

QY	1	GNAERAPGSRSGFVPTLLAAA---LAVSDALGRPSRDEBELVPELRAPGHG--T	55
DB	2	GDVGRARSRSGLSAHMLLILASITMLCARGAHGRTEDEBELVLSERAPHDST	61
QY	56	TRLRLAHPDQOLDELAPDSSFLAPGTLQVNGKSGSETP--PETDLAHCFTGTVNG	113
DB	62	TRLRLDAFGQQLHLKLPDSGLFAPGFTLQTVGRSGSEAOHLDPYGLAHCFTGTVNG	121
QY	114	DPSAALSLCEGVRGAFYLLGEAVFTQPL--AASERLATAAPGKPPAPLOHLLRNR	172
DB	122	DPSAALSLCEGVRGAFYLLQGEFTQPAFVATERLAPVPESSARPOFHLRRR	181
QY	173	QGDVGTGCVVDDEPRPTGKAREDEDEGTEGDEGAQWSPODPALQGVGQPTGTSIRK	232
DB	182	RSGGAKCGVWDDETLPT-----SDSRPSQVTRNQMPVRDPTPODAGKPSGSGIRK	234
QY	233	KRFVSHRYVETMLVADQSMAEFHGSLKHYLLTLPVSAALYKHPISIRNSVLVVKIL	292
DB	235	KRFVSPRYVETMLVADQSMADFHGSLKHYLLTLPVSAALYKHPISIRNSVLVVKIL	294
QY	293	VTHDEQKPEVTSNAALLTRHFCMOKOHNSPRDDEHYTALLFRQDLCGSGTCDTL	352
DB	295	VTHDEQKPEVTSNAALLTRHFCMOKOHNSPRDDEHYTALLFRQDLCGSGTCDTL	354
QY	353	GMADVGTVCDFPSRSCSYIEDGLQAAFTTAHELGHVFEMPHDDAKQCASLGVNDSHM	412
DB	355	GMADVGTVCDFPSRSCSYIEDGLQAAFTTAHELGHVFEMPHDDAKQCASLGVNDSHM	414
QY	413	ASMLSNIDHSQPMSPCAINMTSTFLDNHGECLMDKQNPQLPGDLFGTSYDANROCF	472
DB	415	ASMLSLIDHSQPMSPCAINMTSTFLDNHGECLMDKQNPQLPGDLFGTSYDANROCF	474
QY	473	TFGEHSRHCPRASCTGTMCTGSGGVVQOTGHPMAODTSGEGWMCNGCVNKH	532
DB	475	TFGEHSRHCPRASCTGTMCTGSGGVVQOTGHPMAODTSGEGWMCNGCVNKH	534
QY	533	RKHFDTPFHSGWGMGMDCSRFCGGGVQVYTRBCNPPYKNGKATCEGRVYRSQNL	592
DB	535	MKEHATVHSGWGMGMDCSRFCGGGVQVYTRBCNPPYKNGKATCEGRVYRSQNL	594
QY	593	EDCPDNNKTFREBOCEAHNEFSAFSGSPAVEMIKYAGVSPDKCKLCOAKGIGYF	652
DB	595	EDCPDNNKTFREBOCEAHNEFSAFSGSPAVEMIKYAGVSPDKCKLCOAKGIGYF	654
QY	653	FVLQPKVNDGTPSPDSTSVYQGOCTKACGDRITIDSKKFKDKGCVGNGNSTKKISGS	712
DB	655	FVLQPKVNDGTPSPDSTSVYQGOCTKACGDRITIDSKKFKDKGCVGNGNSTKKISGS	714
QY	713	VTSAPGVYHDIITITPATNIEVKQRQNRSGNNGSLAIKAADGTIYLNDDYTLSTLEQ	772
DB	715	VTSAPGVYHDIITITPATNIEVKQRQNRSGNNGSLAIKAADGTIYLNDDYTLSTLEQ	774
QY	773	DIMTKGVILYSSGSAALERIRSPSLKEPLTIOVLTVGNALRPKIKYTYFVKKKSGFN	832
DB	775	DIMTKGVILYSSGSAALERIRSPSLKEPLTIOVLTVGNALRPKIKYTYFVKKKSGFN	834
QY	833	AIIPFSWVIEEWGEGSKSGELGQORLYVCRDINQPAEBCAKYVPASTRPADHPCP	892
DB	835	AIIPFSWVIEEWGEGSKSGELGQORLYVCRDINQPAEBCAKYVPASTRPADHPCP	894
QY	893	QWOLGWSKSKTGKGRKSLKLSHDPGVLSSHSCDCLKKPKHPIDFCTMAECS	949

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OM protein - protein search, using sw model

Run on: March 17, 2006, 17:51:04 ; Search time 242 seconds
(without alignments)
2766.721 Million cell updates/sec

Title: US-10-667-281-2
Perfect score: 5183
Sequence: 1 GNAERAPGSRSPGVPVTLT.....CDPLKKPKHFDICTMAECS 949

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 10 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	5169	99.7	667 1	ATSI1_HUMAN
2	5164	99.6	967 2	Q9UH18_HUMAN
3	5161	99.6	967 2	Q8HBE26_HUMAN
4	4750	91.6	911 2	Q5R6D5_PONPY
5	4291.5	82.8	968 1	ATSI1_MOUSE
6	4285	82.7	967 2	Q68EJ2_RAT
7	4279	82.6	967 1	Q9WUQ1_RAT
8	3921.5	75.7	759 2	Q8H2M8_HORSE
9	3718	71.7	928 2	Q5U261_XENTIA
10	2512.5	48.5	950 2	Q504Z2_MOUSE

ALIGNMENTS

Result 1
ATSI1_HUMAN STANDARD; PRT; 967 AA.
AC Q9UH18; Q9NSU8; Q9P2K0; Q9UH83; Q9UP80;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE ADAMTS-1 Precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TS1) (METH-1).
GN Name=ADAMTS1; Synonyms=K1A1346, METH1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
NCBI TaxID=9606;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RA Casas C., Pritchard M.A., Bellvill X., Arbones M.L.;
RT "Cloning, characterization and mapping on human chromosome 21 of the
RT orthologue of murine Adamts-1.";
RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE, AND FUNCTION.
RC TISSUE=Heart;
RX MEDLINE=99367466; PubMed=10438512; DOI=10.1074/jbc.274.33.23349;
RA Vazquez F., Hastings G., Ortega M.-A., Lane T.F., Oikemus S.,
RA Lombarco M., Iruela-Arispe M.L.;
RT "METH-1, a human ortholog of ADAMTS-1, and METH-2 are members of a new
RT family of proteins with angio-inhibitory activity.";
RL J. Biol. Chem. 274:23349-23357(1999).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=endothelial cell;
RX MEDLINE=20247184; PubMed=10785405;
RA Glienne J., Schmitt A.O., Pilarsky C., Hinzmann B., Weiss B.,
RA Rosenthal A., Thierach K.H.;
RT "Differential gene expression by endothelial cells in distinct
RT angiogenic states.";
RL Eur. J. Biochem. 267:2820-2830(2000).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain;
RX MEDLINE=20181126; PubMed=10718198;
RA Nagase T., Kakuno R., Ishikawa K.-I., Hirosewa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XVI.
RT The complete sequences of 150 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 7:65-73(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=20289799; PubMed=10830953; DOI=10.1038/35012518;
RA Hattori M., Fujiyama A., Taylor T.D., Matanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Tsuchi T., Choi D.-K., Gromer Y.,
RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Minoshima S., Shimizu N., Nordström G., Horikawa S., Antonarakis S.E.,
RA Schaefer M., Schen O., Desario A., Reichelt J., Kauer G., Bloecher H.,
RA Ransner J., Beck A., Klages S., Hennig S., Rieselmann L., Degand E.,
RA Leinweber S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 418-967.
RC TISSUE=Melanoma;
RG The German cDNA consortium;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cleaves aggrecan, a cartilage proteoglycan, and may be
CC involved in its turnover (By similarity). Has angiogenic inhibitor
CC activity. Active metalloprotease, which may be associated with
CC various inflammatory processes as well as development of cancer
CC cachexia. May play a critical role in follicular rupture.
CC -1- CATALYTIC ACTIVITY: Cleaves aggrecan at the 1938-Glu-|-Leu-1939
CC site, within the chondroitin sulfate attachment domain.
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
CC matrix (By similarity).
CC -1- DOMAIN: The spacer domain and the TSP type-1 domains are important
CC for a tight interaction with the extracellular matrix.
CC -1- PFM: The precursor is cleaved by a furin endopeptidase (By
CC similarity).
CC -1- SIMILARITY: Contains 1 disintegrin domain.
CC -1- SIMILARITY: Contains 1 peptidase M2B domain.
CC -1- SIMILARITY: Contains 3 TSP type-1 domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration

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OM protein - protein search, using sw model

Run on: March 17, 2006, 18:10:45 ; Search time 25 seconds
(without alignments)
1086.525 Million cell updates/sec

Title: US-10-667-281-2

Perfect score: 5173

Sequence: 1 GNAERAPGSRSGFPVPTLL.....CDPLKPKHFDICTMAECS 949

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 10 summaries

Database : Published Applications AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5174	99.8	967	6	US-10-995-561-979 Sequence 979, App
2	5174	99.8	967	6	US-10-995-561-980 Sequence 980, App
3	5174	99.8	999	6	US-10-821-234-1251 Sequence 1251, App
4	5169	99.7	967	7	US-11-169-041-191 Sequence 191, App
5	2334.5	43.0	890	7	US-11-106-623-28 Sequence 28, App1
6	2136	41.2	837	7	US-11-127-877-74 Sequence 74, App1
7	1774	34.2	1076	7	US-11-109-157A-5 Sequence 5, App1
8	1734	33.5	1907	7	US-11-039-398-25 Sequence 25, App1
9	1622.5	31.3	785	7	US-11-109-157A-6 Sequence 6, App1
10	1331	25.7	1686	7	US-11-109-157A-1 Sequence 1, App1

ALIGNMENTS

RESULT 1
US-10-995-561-979
; Sequence 979, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 979
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-979

Query Match 99.8% Score 5174; DB 6; Length 967;
Best Local Similarity 99.9% Pred. No. 0;
Matches 948; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	GNAERAPGSRSGFPVPTLLAAALAVSDALGRSEDEBLVPELRAPGHGTRRL	60
DB	19	GNAERAPGSRSGFPVPTLLAAALAVSDALGRSEDEBLVPELRAPGHGTRRL	78
QY	61	HAFDQDLRLRPSSFLAPGFTLQNVGRKSGSTPLPETDLACFTYSGTVNGDPSAA	120
DB	79	HAFDQDLRLRPSSFLAPGFTLQNVGRKSGSTPLPETDLACFTYSGTVNGDPSAA	138
QY	121	LSLCEGVGAFYLLGEAFYIOPLPASRLATAAAGEPPAPLOPHLLRRRGQGVGTC	180
DB	139	LSLCEGVGAFYLLGEAFYIOPLPASRLATAAAGEPPAPLOPHLLRRRGQGVGTC	198
QY	181	GVNDEPRPTKAETEDDEGEDEBGAQMSPODPALQGVGPTGTSIRKGRFVSSH	240
DB	199	GVNDEPRPTKAETEDDEGEDEBGAQMSPODPALQGVGPTGTSIRKGRFVSSH	258
QY	241	YVEITLVADQMAEFHSGGLKHYLLTFSVAARLYKHPISINVSLLVVKILVIHDEQK	300
DB	259	YVEITLVADQMAEFHSGGLKHYLLTFSVAARLYKHPISINVSLLVVKILVIHDEQK	318
QY	301	PEVTSNALTRNRCNNKONNPSDRAEYDPAIIFTRDLCSSQTCDTLGNADVGV	360
DB	319	PEVTSNALTRNRCNNKONNPSDRAEYDPAIIFTRDLCSSQTCDTLGNADVGV	378
QY	361	CDPSRSCVIEDDGLQAAFTTAHEIGHVFNPHDADAKCASLNGVQDSHMAASLNL	420
DB	379	CDPSRSCVIEDDGLQAAFTTAHEIGHVFNPHDADAKCASLNGVQDSHMAASLNL	438
QY	421	HSQPMSPCSAMVITSLFDNGHGECLMDKPNPDIOLPGDLPSTYDANRCQFTGEDSKH	480
DB	439	HSQPMSPCSAMVITSLFDNGHGECLMDKPNPDIOLPGDLPSTYDANRCQFTGEDSKH	498
QY	481	CPDAASTCTSLMCTGSGVLYCOTKHPMADGTSCEGKWCINGKCNKTRDKHFDTPF	540
DB	499	CPDAASTCTSLMCTGSGVLYCOTKHPMADGTSCEGKWCINGKCNKTRDKHFDTPF	558
QY	541	HSGMGMGPMWDGSCRTGCGGVQYTMRECDNVPKNGGKCEGKRVYRSCNLEDCPDNNG	600
DB	559	HSGMGMGPMWDGSCRTGCGGVQYTMRECDNVPKNGGKCEGKRVYRSCNLEDCPDNNG	618
QY	601	KTFREBOCEANERFSKASFGSGPAVEMIPKXAGVSPKORCLICQAKIGIFPVLPQRYV	660
DB	619	KTFREBOCEANERFSKASFGSGPAVEMIPKXAGVSPKORCLICQAKIGIFPVLPQRYV	678
QY	661	DGTFCSPDSTSVCCQGCVRAGCRRITDSKKKPKCGVCGSGNSTCKKISSVYSARKGY	720
DB	679	DGTFCSPDSTSVCCQGCVRAGCRRITDSKKKPKCGVCGSGNSTCKKISSVYSARKGY	738
QY	721	HDITITPTGATNIEVKORNGSRNNGSFLAIKADGTIILNGDYTLSTLRODITKGV	780
DB	739	HDITITPTGATNIEVKORNGSRNNGSFLAIKADGTIILNGDYTLSTLRODITKGV	798
QY	781	LRYGSSAALERIRISFPLKEPLTIQVLYVGNALRPKIXTYFYKKKSSFNALPTFSAM	840
DB	799	LRYGSSAALERIRISFPLKEPLTIQVLYVGNALRPKIXTYFYKKKSSFNALPTFSAM	858
QY	841	VIEWEGSCSKSCELGQWRVLVECDINGOPASBECAKXVPASTPCADHPPOWLGWS	900
DB	859	VIEWEGSCSKSCELGQWRVLVECDINGOPASBECAKXVPASTPCADHPPOWLGWS	918

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OM protein - protein search, using sw model

Run on: March 17, 2006, 18:09:50 ; Search time 169 Seconds
(without alignments)
2346.272 Million cell updates/sec

Title: US-10-667-281-2
Perfect score: 5183
Sequence: 1 GNAERAPGSRSPGVPTLL.....CDPLKPKHFDCTMAECS 949

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 10 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5183	100.0	949	US-10-667-281-2	Sequence 2, Appli
2	5174	99.8	950	US-10-741-600-1605	Sequence 1605, Ap
3	5174	99.8	950	US-10-973-858-14	Sequence 14, Appl
4	5174	99.8	967	US-10-741-600-1603	Sequence 1603, Ap
5	5174	99.8	967	US-10-741-600-1604	Sequence 1604, Ap
6	5174	99.8	967	US-10-923-035-37	Sequence 37, Appl
7	5174	99.8	967	US-10-756-149-5619	Sequence 5619, Ap
8	5169	99.7	950	US-09-373-658-2	Sequence 2, Appli
9	5169	99.7	950	US-09-989-687-2	Sequence 2, Appli
10	5169	99.7	967	US-10-105-929-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-667-281-2
; Sequence 2, Application US/10667281
; Publication No. US20050100916A1
; GENERAL INFORMATION:
; APPLICANT: Klonowski, Paul
; APPLICANT: Allard, John
; APPLICANT: Heller, Renu
; APPLICANT: Van Walt, Harold
; TITLE OF INVENTION: Human Aggrecanase and Nucleic Acid
; TITLE OF INVENTION: Compositions Encoding the Same
; FILE REFERENCE: ROCH-002

Q	1	GNAERAPGSRSPGVPTLLAAALAVSDALGRSEDEBELVPELERAPGHGTTURL	60
Q	1	GNAERAPGSRSPGVPTLLAAALAVSDALGRSEDEBELVPELERAPGHGTTURL	60
Q	61	HAFOQDLLELRPDSSFLAPGFTLONVGRKSSFTPLBETDLACFTYSGTVNGDPSAAA	120
Q	61	HAFOQDLLELRPDSSFLAPGFTLONVGRKSSFTPLBETDLACFTYSGTVNGDPSAAA	120
Q	121	LSICGVGAFYLLGEAYFIOPPLPASERLTAARCEPAPLOPHLLRNNOGVGCTC	180
Q	121	LSICGVGAFYLLGEAYFIOPPLPASERLTAARCEPAPLOPHLLRNNOGVGCTC	180
Q	181	GVNDDEPRPTGAETDEDEDEGEDEGAQMSPODPAQGVQPTGTSIRKKRFVSSH	240
Q	181	GVNDDEPRPTGAETDEDEDEGEDEGAQMSPODPAQGVQPTGTSIRKKRFVSSH	240
Q	241	YVETMLVADQSMAEFHSGGLKHYLLTFSVAARLYKHSINNSVLVVKILVIHDEQK	300
Q	241	YVETMLVADQSMAEFHSGGLKHYLLTFSVAARLYKHSINNSVLVVKILVIHDEQK	300
Q	301	PEVTSNALTLRNFCNMOKHNPESDRDAEHYDTALFTPRODLSGSGTCDTLGMAVGV	360
Q	301	PEVTSNALTLRNFCNMOKHNPESDRDAEHYDTALFTPRODLSGSGTCDTLGMAVGV	360
Q	361	CDPSRSCVIEDDGLQAAFTTAHELGHVFNMPHDQAKOCASINGVODSHMAASMLNLD	420
Q	361	CDPSRSCVIEDDGLQAAFTTAHELGHVFNMPHDQAKOCASINGVODSHMAASMLNLD	420
Q	421	HSQWSPCSAYMTTSTFLDNGHGECLMDKPNPDIQLPGLPGTSYDANROCOFTFEDSKH	480
Q	421	HSQWSPCSAYMTTSTFLDNGHGECLMDKPNPDIQLPGLPGTSYDANROCOFTFEDSKH	480
Q	481	CPDAASTCTLMCTGSGVAVCOTKHPMAADGTSCEGKXKCNKVKTHRKHPDPF	540
Q	481	CPDAASTCTLMCTGSGVAVCOTKHPMAADGTSCEGKXKCNKVKTHRKHPDPF	540
Q	541	HGSMGMGPMWDCSRTCGGAVQYTMRECDNVPVXNGKXCEGKRVYRSCNLEDCPDNNG	600
Q	541	HGSMGMGPMWDCSRTCGGAVQYTMRECDNVPVXNGKXCEGKRVYRSCNLEDCPDNNG	600
Q	601	KTFREOCEAHNEFSKASFGSGPAVEMIPKTAGVSPKORCLICQAKIGYFVLQPKV	660
Q	601	KTFREOCEAHNEFSKASFGSGPAVEMIPKTAGVSPKORCLICQAKIGYFVLQPKV	660
Q	661	DGTPSPSTSVCCVQGCCKRITDSKKKPKCGVCGNGSGTCKTSSGVSATKGY	720
Q	661	DGTPSPSTSVCCVQGCCKRITDSKKKPKCGVCGNGSGTCKTSSGVSATKGY	720
Q	721	HDITITPGATNIEVKQNRGSRNGSFLAIKADGTYYLNGDYTLSTLEODIMYKGV	780
Q	721	HDITITPGATNIEVKQNRGSRNGSFLAIKADGTYYLNGDYTLSTLEODIMYKGV	780
Q	781	LYSGSSAALERRISFSPLEKPLTIOVLTGNALRPKIKYTYFYKKGKESRAIYTSAM	840
Q	781	LYSGSSAALERRISFSPLEKPLTIOVLTGNALRPKIKYTYFYKKGKESRAIYTSAM	840

CURRENT APPLICATION NUMBER: US/10/667,281
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/568,559
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: 60/133,343
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 949
; TYPE: PRT
; ORGANISM: human
US-10-667-281-2

Query Match 100.0%; Score 5183; DB 5; Length 949;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 949; Conservative 0; Mismatches 0; Indels 0; Gaps 0;